

WO 00/26372

PCT/US99/26177

## SEQUENCE LISTING

&lt;110&gt; INCYTE PHARMACEUTICALS, INC.

TANG, Y. Tom  
 CORLEY, Neil C.  
 GORGONE, Gina A.  
 GUEGLER, Karl J.  
 BAUGHN, Mariah R.

&lt;120&gt; MYOSIN HEAVY CHAIN HOMOLOG

&lt;130&gt; PF-0621 PCT

&lt;140&gt; To Be Assigned

&lt;141&gt; Herewith

&lt;150&gt; 09/187,060; unassigned

&lt;151&gt; 1998-11-05; 1998-11-05

&lt;160&gt; 4

&lt;170&gt; PERL Program

&lt;210&gt; 1

&lt;211&gt; 612

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: 1929760CD1

&lt;400&gt; 1

Met	Phe	Cys	Pro	Pro	Gln	Val	Ser	Cys	Ser	Leu	Ser	Leu	Met	Pro
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Arg	Leu	Pro	Ser	Ile	Arg	His	Trp	Gln	Gly	Pro	Ser	His	Pro	Gly
				20					25					30
Phe	Leu	Gly	Pro	Leu	Phe	Pro	Ile	Cys	Ser	Leu	Gln	Trp	Pro	His
				35					40					45
Gly	Phe	Ser	Ala	Ile	Phe	Pro	Gly	Leu	Leu	Asp	Val	Tyr	Gly	Phe
				50					55					60
Glu	Ser	Phe	Pro	Asp	Asn	Ser	Leu	Glu	Gln	Leu	Cys	Ile	Asn	Tyr
				65					70					75
Ala	Asn	Glu	Lys	Leu	Gln	Gln	His	Phe	Val	Ala	His	Tyr	Leu	Arg
				80					85					90
Ala	Gln	Gln	Glu	Glu	Tyr	Ala	Val	Glu	Gly	Leu	Glu	Trp	Ser	Phe
				95					100					105
Ile	Asn	Tyr	Gln	Asp	Asn	Gln	Pro	Cys	Leu	Asp	Leu	Ile	Glu	Gly
				110					115					120
Ser	Pro	Ile	Ser	Ile	Cys	Ser	Leu	Ile	Asn	Glu	Glu	Cys	Arg	Leu
				125					130					135
Asn	Arg	Pro	Ser	Ser	Ala	Arg	Gln	Leu	Gln	Thr	Arg	Ile	Glu	Thr
				140					145					150
Ala	Leu	Ala	Gly	Ser	Pro	Cys	Leu	Gly	His	Asn	Lys	Leu	Ser	Arg

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	155		160		165
Glu Pro Ser Phe	Ile Val Val His Tyr	Ala Gly Pro Val Arg Tyr			
	170		175		180
His Thr Ala Gly	Leu Val Glu Lys Asn	Lys Asp Pro Ile Pro Pro			
	185		190		195
Glu Leu Thr Arg	Leu Leu Gln Gln Ser	Gln Asp Pro Leu Leu Met			
	200		205		210
Gly Leu Phe Pro	Thr Asn Pro Lys Glu	Lys Thr Gln Glu Glu Pro			
	215		220		225
Pro Gly Gln Ser	Arg Ala Pro Val Leu	Thr Val Val Ser Lys Phe			
	230		235		240
Lys Ala Ser Leu	Glu Gln Leu Leu Gln	Val Leu His Ser Thr Thr			
	245		250		255
Pro His Tyr Ile	Arg Cys Ile Lys Pro	Asn Ser Gln Gly Gln Ala			
	260		265		270
Gln Thr Phe Leu	Gln Glu Glu Val Leu	Ser Gln Leu Glu Ala Cys			
	275		280		285
Gly Leu Val Glu	Thr Ile His Ile Ser	Ala Ala Gly Phe Pro Ile			
	290		295		300
Arg Val Ser His	Arg Asn Phe Val Glu	Arg Tyr Lys Leu Leu Arg			
	305		310		315
Arg Leu His Pro	Cys Thr Ser Ser Gly	Pro Asp Ser Pro Tyr Pro			
	320		325		330
Ala Lys Gly Leu	Pro Glu Trp Cys Pro	His Ser Glu Glu Ala Thr			
	335		340		345
Leu Glu Pro Leu	Ile Gln Asp Ile Leu	His Thr Leu Pro Val Leu			
	350		355		360
Thr Gln Ala Ala	Ala Ile Thr Gly Asp	Ser Ala Glu Ala Met Pro			
	365		370		375
Ala Pro Met His	Cys Gly Arg Thr Lys	Val Phe Met Thr Asp Ser			
	380		385		390
Met Leu Glu Leu	Leu Glu Cys Gly Arg	Ala Arg Val Leu Glu Gln			
	395		400		405
Cys Ala Arg Cys	Ile Gln Gly Gly Trp	Arg Arg His Arg His Arg			
	410		415		420
Glu Gln Glu Arg	Gln Trp Arg Ala Val	Met Leu Ile Gln Ala Ala			
	425		430		435
Ile Arg Ser Trp	Leu Thr Arg Lys His	Ile Gln Arg Leu His Ala			
	440		445		450
Ala Ala Thr Val	Ile Lys Arg Ala Trp	Gln Lys Trp Arg Ile Arg			
	455		460		465
Met Ala Cys Leu	Ala Ala Lys Glu Leu	Asp Gly Val Glu Glu Lys			
	470		475		480
His Phe Ser Gln	Ala Pro Cys Ser Leu	Ser Thr Ser Pro Leu Gln			
	485		490		495
Thr Arg Leu Leu	Glu Ala Ile Ile Arg	Leu Trp Pro Leu Gly Leu			
	500		505		510
Val Leu Ala Asn	Thr Ala Met Gly Val	Gly Ser Phe Gln Arg Lys			
	515		520		525
Leu Val Val Trp	Ala Cys Leu Gln Leu	Pro Arg Gly Ser Pro Ser			
	530		535		540
Ser Tyr Thr Val	Gln Thr Ala Gln Asp	Gln Ala Gly Val Thr Ser			
	545		550		555
Ile Arg Ala Leu	Pro Gln Gly Ser Ile	Lys Phe His Cys Arg Lys			
	560		565		570

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Ser	Pro	Leu	Arg	Tyr	Ala	Asp	Ile	Cys	Pro	Glu	Pro	Ser	Pro	Tyr
				575					580					585
Ser	Ile	Thr	Gly	Phe	Asn	Gln	Ile	Leu	Leu	Glu	Arg	His	Arg	Leu
				590					595					600
Ile	His	Val	Thr	Ser	Ser	Ala	Phe	Thr	Gly	Leu	Gly			
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<210> 2

<211> 2109

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: 1929760CB1

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accacaggtg	tcatgctcac	tcagcctgat	gccagggctg	ccaagtataa	ggcattggca	180
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ccatgggttc	tctgccatct	tcccaggcct	gctggatgtg	tatggatttg	aatcatttcc	300
tgacaacagt	ctggaacagt	tgtgcatcaa	ctacgccaat	gagaagctgc	agcagcattt	360
tgtggctcac	tacctaaagg	cccagcagga	ggaatacgca	ggtgagggcc	tggagtgggc	420
attcatcaac	taccaggaca	accagccctg	tttggatctc	attgagggaa	gccccatcag	480
catctgctcc	ctcataaatg	aggaatgccg	cctcaatcga	cccagcagcg	cacgccagct	540
ccagacacgc	attgagactg	ccctggcagg	cagccccctg	ctgggccaca	ataagctcag	600
ccgggagccc	agcttcattg	tgggtgcatta	tgcggggcct	gtgcggtacc	acacagcagg	660
cctgggtggag	aagaacaagg	accctatccc	acctgagctg	accaggctcc	tgagcaaatc	720
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gcagtgtgcc	cgctgcatcc	aggggtggctg	gaggcgacac	cggcaccgag	agcaggagcg	1380
gcagtggcgg	gccgtcatgc	tcatccaggc	agccattcgt	tcctgggtta	ctcggaatac	1440
catccagagg	ctgcatgcag	ctgccacagt	catcaagcgt	gcattggcaga	agtggagaat	1500
cagaatggcc	tgcccttgctg	ctaaaagagct	ggatgggtgtg	gaagaaaaaac	acttctctca	1560
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cctctggccc	ctgggactgg	tcctggccaa	tacggctatg	ggtgtaggca	gctttcagag	1680
gaaattagtg	gtctgggctt	gcctccagct	ccccaggggc	agccccagta	gctacactgt	1740
ccagacagca	caagaccagg	ctgggtgtcac	gtccatccga	gcgctgcctc	agggatcgat	1800
aaagtttcac	tgagaaaagt	ctccactgcg	gtatgctgac	atctgccttg	aaccttcacc	1860
ctacagcatt	acaggcttta	atcagattct	gctggaaaaga	cacaggctga	tccacgtgac	1920
ctcttctgcc	ttcactgggc	tgggggtgatc	cttgggtgcct	ttgtttccac	aaggcctttt	1980
cctgccccct	gccttgccaa	agacattttaa	tcagcacaca	gctgccagac	tattcccaca	2040
gtgctccaaa	tgacatgaa	caacagtgc	ggctccagcc	ttcgaccag	agccccgtgc	2100
ccagtgcgt						2109

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<210> 3  
 <211> 1839  
 <212> PRT  
 <213> Caenorhabditis elegans

<300>  
 <308> GenBank ID No: g1279777

<400> 3  
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 Pro Asn Arg Lys Lys Ile Gly Ser Ile Gln Tyr Gly Arg Arg Arg  
 20 25 30  
 His Ser Trp Gln Gly Pro Val Val Pro Ala Lys Leu Gln Val  
 35 40 45  
 Leu Ile Lys Gly Val Arg Ile Trp His Arg His Pro Thr Leu Val  
 50 55 60  
 Trp Ile Gly Ala Thr Leu Glu Glu Asp Ile Thr Phe Gln Thr Arg  
 65 70 75  
 Asn Val Arg Ile Arg Leu Glu Asp Asp Thr Glu Val Glu Tyr Ala  
 80 85 90  
 Ile Lys Ser Leu Asp Gln Leu Pro Phe Leu Arg Asn Pro Ala Phe  
 95 100 105  
 Leu Val Gly Lys Asp Asp Leu Thr Leu Leu Ser Tyr Leu His Glu  
 110 115 120  
 Pro Ala Val Leu His Asn Leu Gln Val Arg Phe Val Lys Gly Ser  
 125 130 135  
 Ser Ile Tyr Thr Tyr Cys Gly Ile Val Leu Val Ala Ile Asn Pro  
 140 145 150  
 Tyr Ala Asp Cys Ser His Ile Tyr Gly Glu Glu Ile Ile Gln Val  
 155 160 165  
 Tyr Arg Gly Ala Gly Lys Ser Ala Arg Glu Met Asp Pro His Ile  
 170 175 180  
 Phe Ala Val Ala Glu Glu Ala His Phe Asp Met Gly Ala Phe Gly  
 185 190 195  
 Lys Ser Gln Ser Ile Ile Val Ser Gly Glu Ser Gly Ala Gly Lys  
 200 205 210  
 Thr Val Ser Ala Lys Phe Val Met Arg Tyr Leu Ala Ser Val Ala  
 215 220 225  
 Ala Ser Lys Thr Arg Asn Gly Gly Thr Thr Ser Ile Glu Ala Arg  
 230 235 240  
 Val Leu Ala Ser Asn Pro Ile Met Glu Ser Ile Gly Asn Ala Lys  
 245 250 255  
 Thr Ile Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Gln  
 260 265 270  
 Ile Asn Phe Cys Glu Arg Gly Arg Arg Ile Val Gly Ala Glu Met  
 275 280 285  
 Lys Thr Tyr Leu Leu Glu Lys Ser Arg Leu Val Phe Gln Ala Pro  
 290 295 300  
 Gly Glu Arg Asn Tyr His Ile Phe Tyr Gln Leu Cys Ala Ala Arg  
 305 310 315  
 Asn His Gln Val Leu Lys Asp Leu His Leu Gly Pro Cys Glu Ser  
 320 325 330  
 Tyr Ser Tyr Leu Thr Gln Gly Gly Asp Ser Arg Ile Pro Gly Val

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Asp Asp Lys Ala	335	Leu Lys Ala Leu	340	Gln Leu	345
Leu Gly Phe Asp	350	Asp Val Phe Arg	355	Leu Leu	360
Ala Gly Leu Leu	365	His Phe Glu Asn	370	Gly Glu	375
Gly Ser Ser Ala	380	Cys Gln Glu Ile	385	Ser Arg	390
Leu Cys Arg Glu	395	Glu Ser Asp Leu	400	Arg Ile	405
Trp Leu Thr Arg	410	Val Asn Glu Ile	415	Val Thr	420
Lys Pro Leu Thr	425	Arg Ser Arg Asp	430	Ala Leu	435
Thr Lys Met Leu	440	Gly Trp Leu Val	445	Asp Lys	450
Ile Asn Glu Ala	455	Lys Leu Asp Gly	460	Thr Asn	465
Gln Lys Lys Arg	470	Gly Val Leu Asp	475	Ile Tyr	480
Gly Phe Glu Thr	485	Phe Glu Gln Phe	490	Ser Ile	495
Asn Tyr Ala Asn	500	Gln Phe Asn Gln	505	His Val	510
Phe Lys Leu Glu	515	Arg Glu Glu Ile	520	Glu Trp	525
Val Arg Val Asp	530	Pro Ala Ile Asp	535	Leu Ile	540
Glu Gly Pro Val	545	Leu Asp Glu Gln	550	Cys Lys	555
Arg Leu Asn Gly	560	Leu Ser Gln Leu	565	Gln Asn	570
Ser Thr Glu Leu	575	Leu Ala Phe Pro	580	Lys Val	585
Arg Ser Asn Asp	590	Phe Ala Ala Asp	595	Val Thr	600
Tyr Ser Thr Asp	605	Gly Phe Val Glu	610	Lys Thr	615
Glu Gln Leu Leu	620	Asn Arg Asp Ala	625	Ile Gly	630
Arg Thr Val Ile	635	Ser Lys Phe Pro	640	Phe Ile	645
Ser Ser Ser Ser	650	Thr Ser Val Ser	655	Ser Ser	660
Ala Ser Gln Phe	665	Thr Ile Lys Lys	670	Thr Val	675
Cys Ser Thr Arg	680	Glu Leu Met Ser	685	Val Leu	690
Ser Lys Ile Ser	695	Cys Ile Lys Pro	700	Asn Asp	705
Leu Arg Ala Cys	710	Lys Arg Ala Ile	715	Gln Gln	720
Gly Phe Pro Ser	725	Val Arg Ile Ser	730	Ala Ala	735
	740	Glu Phe Ala Arg	745	Arg Tyr	750

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Arg	Val	Ile	Tyr	Thr	Lys	Glu	Ala	Ala	Leu	Trp	Arg	Asp	Lys	Pro
				755					760					765
Lys	Gln	Phe	Ala	Glu	Leu	Ala	Cys	Gln	Gln	Cys	Leu	Glu	Glu	Gly
				770					775					780
Lys	Tyr	Ala	Val	Gly	Lys	Thr	Lys	Ile	Phe	Leu	Arg	Thr	Gly	Gln
				785					790					795
Val	Ala	Val	Leu	Glu	Arg	Val	Arg	Leu	Asp	Thr	Leu	Ala	Ala	Ala
				800					805					810
Ala	Thr	Val	Ile	Gln	Lys	Met	Trp	Lys	Gly	Phe	Leu	Ala	Arg	Arg
				815					820					825
Lys	Tyr	Glu	Thr	Met	Arg	Arg	Ser	Leu	Leu	Ile	Val	Gln	Ala	Ser
				830					835					840
Leu	Lys	Ala	Phe	Leu	Ala	Phe	Arg	Arg	Ile	Lys	Tyr	Leu	Gln	Met
				845					850					855
His	Arg	Ala	Val	Ile	Val	Met	Gln	Ser	Ala	Val	Arg	Gly	Tyr	Leu
				860					865					870
Glu	Arg	Arg	Lys	Tyr	Glu	Gln	Ile	Arg	Asp	Ser	Ile	Ile	Gly	Ile
				875					880					885
Gln	Ala	Met	Phe	Lys	Ala	Asn	Arg	Val	Arg	Arg	Tyr	Val	Glu	Lys
				890					895					900
Leu	Arg	Tyr	Glu	Lys	Ser	Ala	Ile	Thr	Ile	Gln	Ala	Ala	Trp	Arg
				905					910					915
Gly	Tyr	Leu	Ala	Arg	Arg	Glu	Gln	Ile	Ala	Asn	Arg	Lys	Lys	Val
				920					925					930
Val	Met	Val	Gln	Cys	Ala	Val	Arg	Lys	Trp	Leu	Ala	Lys	Arg	Arg
				935					940					945
Leu	Arg	Glu	Leu	Lys	Ile	Glu	Ala	Arg	Ser	Val	Gly	His	Leu	Gln
				950					955					960
Lys	Leu	Asn	Thr	Gly	Leu	Glu	Asn	Lys	Ile	Ile	Glu	Leu	Gln	Met
				965					970					975
Arg	Leu	Asp	Ile	Ala	Asn	Ala	Arg	Thr	Lys	Glu	Glu	Ala	Glu	Lys
				980					985					990
Phe	Ala	Thr	Ala	Ser	Lys	Asn	Leu	Gln	Lys	Thr	Lys	Ala	Asp	Leu
				995					1000					1005
Ala	Met	Met	Glu	Ala	Glu	Arg	Leu	Thr	Leu	Leu	Glu	Ala	Arg	Asn
				1010					1015					1020
Arg	Val	Glu	Val	Leu	Gln	Glu	Glu	Val	Glu	Arg	Leu	Glu	Thr	Glu
				1025					1030					1035
Cys	Asp	Leu	Lys	Glu	Ala	Gln	Arg	Gly	Gly	Met	Glu	Thr	Lys	Met
				1040					1045					1050
Val	Glu	Leu	Gln	Ser	Arg	Leu	Asp	Gln	Phe	Gln	Met	Gln	Ser	Glu
				1055					1060					1065
Ser	Gly	Gln	Thr	Ile	Val	Glu	Leu	Thr	Glu	Gln	Leu	Glu	Lys	Ala
				1070					1075					1080
Lys	Ala	Asp	Arg	Val	Leu	Trp	Asp	Glu	Glu	Arg	Gln	Arg	Met	Glu
				1085					1090					1095
Ala	Ala	Leu	Asn	Thr	Glu	Arg	Ser	Ala	Arg	Asn	Ala	Leu	Asp	Ala
				1100					1105					1110
Glu	Met	Ala	Ala	Met	Arg	Glu	Gln	Leu	Met	Lys	Asn	Val	Asp	Leu
				1115					1120					1125
Phe	Glu	Ser	Ser	Thr	Phe	Gln	Lys	Arg	Pro	Ser	Gln	Lys	Lys	Asn
				1130					1135					1140
Arg	Asp	Asp	Asp	Ser	Cys	Ser	Arg	Thr	Thr	Ser	Asn	Leu	Ser	Gln
				1145					1150					1155
Leu	Thr	Gly	Ser	Phe	Thr	Ala	Glu	Thr	Ile	Asn	Gly	Val	His	Ser

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1160	1165	1170
Thr Ser Arg Gly Ser Pro Glu Val Leu Leu Asp Asn Met Ala Ser		
1175	1180	1185
Thr Phe Glu Gln Leu Arg Met Ile Asn Asp Leu Arg Gln Arg Asn		
1190	1195	1200
Glu His Cys Gln Arg Glu Thr Glu Arg Met Lys Ala Ile Ile Glu		
1205	1210	1215
Ala Ser Thr Leu Ile Glu Thr Leu Asp Lys Lys Thr Ser Leu Lys		
1220	1225	1230
Ala Phe Glu Ser Ile Arg Val Gly Glu Leu Glu Gly Ala Tyr Asn		
1235	1240	1245
Arg Leu Lys Asn Asp Met Glu Arg Leu Val Ser Gly Glu Asn Gly		
1250	1255	1260
Ala Thr His Ser Val Phe Glu Arg Ile Met Glu Glu Asn Glu Arg		
1265	1270	1275
Leu Arg Glu Glu Ala Val Glu Leu Arg Ser Met Leu Ser Ser His		
1280	1285	1290
Phe Glu Lys Gln Ser Val Ala Gly Ser Ser Gly Tyr Arg Arg Ser		
1295	1300	1305
Pro Arg Pro Asp Ser Gly His Cys Ser Gly Ala Asp Ser Glu Asp		
1310	1315	1320
Gly Ser Ser Gly Ala Asp Leu Glu Glu Asp Leu Cys Ile Glu Arg		
1325	1330	1335
Gln Cys Arg His Leu Lys Asn Leu Ala Glu Asn Leu Thr Lys Met		
1340	1345	1350
Leu Thr Asn Gln Asn Leu Glu Ile Glu Arg Leu Gln Gln Gln Leu		
1355	1360	1365
Arg Phe Ser Glu Ser Gln Thr Val Phe Arg Pro Ser Asp Cys Ser		
1370	1375	1380
Leu Asp Glu Ala Val Arg Gly Ala His Lys Gln Thr Gln Leu Leu		
1385	1390	1395
Ala Gln Gln Asn Met Asp Leu Asn Asp Lys Leu Thr Arg Gln Ser		
1400	1405	1410
Glu Glu Leu Ala Glu Ala Arg Ala Gln Leu Arg Gly Tyr Ser Gly		
1415	1420	1425
Pro Leu Gly Leu Glu Asn Ala Ser Asp Glu Glu Ile Ile Arg Leu		
1430	1435	1440
Glu Ala Phe Glu Lys Gly Ser Ile Lys His Ser Gly Phe Leu Glu		
1445	1450	1455
Val Tyr Asn Val Pro Glu Phe Ala Arg Ile Ile Val Cys Glu Leu		
1460	1465	1470
Lys Pro Thr Leu Ala Arg Leu Leu Thr Lys Asn Leu Pro Ala Tyr		
1475	1480	1485
Leu Leu Val Ala Ala Phe Arg Asn His Asp Glu Lys Arg Asp Glu		
1490	1495	1500
Thr Ala Leu Thr Gly Leu Phe Ser Ser Val His Leu Val Leu Lys		
1505	1510	1515
Asp Thr Ile Ser Arg Ser His Asp Leu Asp Leu Leu Ser Leu Trp		
1520	1525	1530
Leu Val Asn Leu Trp Arg Leu Phe Asn Leu Leu Arg Gln Tyr Ser		
1535	1540	1545
Gly Glu Asp Ser Gln Pro Glu Trp His Val Ala Asn Thr Glu Thr		
1550	1555	1560
Gln Asn Ser Tyr Arg Phe Lys Ala Tyr Asp Val Ala Pro Ile Arg		
1565	1570	1575

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Asp Gln Leu Lys Leu Arg Ile Glu Glu Cys Tyr Thr Ser Leu Met  
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 Lys Lys Ala Ile Glu His Val Leu Ser Pro Lys Ile Val Pro Gly  
 1595 1600 1605  
 Ile Leu Gln His Glu Ser Ser Ser Asp Leu Met Thr Ala Gly Gln  
 1610 1615 1620  
 Glu Arg Arg Asp Arg Asn Ser Gly Ser Val Glu Ser Gln Arg Lys  
 1625 1630 1635  
 Ser Leu Asp Asp Leu Leu Gln Phe Met Glu Ile Val His Thr Lys  
 1640 1645 1650  
 Leu Thr Thr Tyr Gly Gly Asp Asp Ile Val Val Lys Gln Val Ile  
 1655 1660 1665  
 Gly Gln Met Ala Arg Trp Met Cys Ala Leu Ala Leu Asn Tyr Met  
 1670 1675 1680  
 Met Phe Arg Arg Glu Leu Cys Asn Phe Glu Lys Ala Ile Gln Ile  
 1685 1690 1695  
 Lys His Asn Val Thr Gln Ile Gln Asn Trp Leu Asn Ala Lys Gly  
 1700 1705 1710  
 Leu Ser Asp Cys Arg Asp His Phe Glu Pro Leu Val Gln Ala Cys  
 1715 1720 1725  
 His Leu Leu Gln Ser Arg Lys Asp Pro Ser Asn Leu Asp Thr Leu  
 1730 1735 1740  
 Cys Gly Glu Met Thr Ser Arg Leu Lys Pro Arg Gln Val Val Ala  
 1745 1750 1755  
 Ile Leu Gln His Tyr Asp Pro Ser Asp Glu Met Glu Asp Gly Leu  
 1760 1765 1770  
 Ser Pro Glu Phe Leu Val Gln Ile Gln Lys Lys Leu Asn Glu Arg  
 1775 1780 1785  
 Ala Ile Ala Asn Asn Asp Pro Ile Glu Asp Lys Asp Lys Leu Ile  
 1790 1795 1800  
 Met Leu Gly Thr Tyr Leu Pro Pro Phe Asp Thr Gln Pro Phe Ser  
 1805 1810 1815  
 Tyr Ser Asp Phe Pro Leu Glu Thr Leu Ser Leu Pro Ser Cys Leu  
 1820 1825 1830  
 His Met Gln Ser Val Cys Arg Leu Val  
 1835

&lt;210&gt; 4

&lt;211&gt; 1120

&lt;212&gt; PRT

&lt;213&gt; Helianthus annuus

&lt;300&gt;

&lt;308&gt; GenBank ID No: g2444174

&lt;400&gt; 4

Met Asp Arg Val Val Asp Asp Asp Ser Pro Tyr Gly Gln Gly Ser  
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 Ser Phe Leu Leu Asn Asp Arg Pro Ser Val Asp Asp Val Asn Asp  
 20 25 30  
 Asp Asp Asp Ala Asp Val Asn Pro Ser Val Ser Ala Gln Gly Ser  
 35 40 45  
 Val Leu Gly Ser Trp Gly Asn Lys Lys Trp Gly Asp Thr Ala Ser



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	50		55		60
Tyr Ile Ala Lys Lys Lys Leu Gln Ser Trp Phe Gln Thr Ser Asp					
	65		70		75
Gly Asn Trp Glu Leu Ala Lys Ile Leu Ser Ile Thr Gly Ser Glu					
	80		85		90
Ser Leu Met Ser Leu Ser Glu Glu Lys Val Leu Lys Val Ser Ser					
	95		100		105
Asp Ser Leu Leu Pro Ala Asn Pro Glu Ile Leu Asp Gly Val Asp					
	110		115		120
Asp Leu Met Gln Leu Ser Tyr Leu Asn Glu Pro Ser Val Leu Tyr					
	125		130		135
Asn Leu Gln Tyr Arg Tyr Asp Arg Asp Met Ile Tyr Ser Lys Ala					
	140		145		150
Gly Pro Val Leu Val Ala Ile Asn Pro Phe Lys Lys Ile Pro Leu					
	155		160		165
Tyr Gly Ser Asp Tyr Ile Glu Ala Tyr Lys Arg Lys Ser Ile Asp					
	170		175		180
Asn Pro His Val Tyr Ala Ile Ala Asp Thr Ala Ile Arg Glu Met					
	185		190		195
Ile Arg Asp Glu Val Asn Gln Ser Ile Val Ile Ser Gly Glu Ser					
	200		205		210
Gly Ala Gly Lys Thr Glu Thr Pro Lys Ile Ala Met Gln Tyr Leu					
	215		220		225
Ala Ala Leu Gly Gly Gly Asp Ala Arg Glu Ser Gly Ile Leu Ser					
	230		235		240
His Asn Gly Cys Arg Thr Pro Arg Arg Ala Glu Ala Phe Gly Asn					
	245		250		255
Ala Lys Thr Ser Arg Asp Asn Asn Ser Ser Arg Ile Gly Lys Leu					
	260		265		270
Ile Glu Ile His Phe Ser Glu Thr Gly Lys Ile Ser Gly Ala Lys					
	275		280		285
Ile Gln Thr Phe Leu Leu Glu Lys Ser Arg Val Val Gln Cys Thr					
	290		295		300
Asp Gly Glu Arg Ser Tyr His Ser Phe Tyr Gln Leu Cys Ala Gly					
	305		310		315
Ala Pro Pro Ser Leu Arg Glu Lys Leu Asn Leu Lys Ser Ala Arg					
	320		325		330
Glu Tyr Lys Tyr Phe Gln Gln Ser Thr Cys Tyr Ser Ile Asn Gly					
	335		340		345
Val Asp Asp Ala Glu Glu Phe Arg Val Val Val Glu Ala Leu Asp					
	350		355		360
Ala Val His Val Ser Lys Glu Asn Gln Glu Asn Ala Phe Ala Met					
	365		370		375
Leu Ala Ala Val Leu Trp Leu Gly Asn Val Thr Phe Ser Ile Val					
	380		385		390
Asp Asn Glu Asn His Val Glu Pro Ile Ile Asp Asp Ala Leu Leu					
	395		400		405
Asn Val Ala Lys Leu Ile Gly Cys Glu Ala Asp Asp Leu Lys Leu					
	410		415		420
Ala Leu Ser Thr Arg Asn Met Lys Val Gly Asn Asp Ile Ile Val					
	425		430		435
Gln Lys Leu Thr Leu Ala Gln Ala Ile Asp Thr Arg Asp Ala Leu					
	440		445		450
Ala Lys Ser Ile Tyr Ser Cys Leu Phe Asp Trp Leu Val Glu Gln					
	455		460		465

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Ile Asn Lys Ser	Leu Ala Val Gly Lys	Arg Arg Thr Gly Arg Ser	
	470	475	480
Ile Ser Ile Leu	Asp Ile Tyr Gly Phe	Glu Ser Phe Asp Val Asn	
	485	490	495
Ser Phe Glu Gln	Phe Cys Ile Asn Tyr	Ala Asn Glu Arg Leu Gln	
	500	505	510
Gln His Phe Asn	Arg His Leu Phe Lys	Leu Glu Gln Glu Glu Tyr	
	515	520	525
Ile Gln Asp Gly	Ile Asp Trp Ala Lys	Val Asp Phe Glu Asp Asn	
	530	535	540
Gln Asp Cys Leu	Asn Leu Phe Glu Lys	Lys Pro Leu Gly Leu Met	
	545	550	555
Thr Leu Leu Asp	Glu Glu Ser Thr Phe	Pro Asn Gly Thr Asp Met	
	560	565	570
Thr Phe Ala Thr	Lys Leu Lys Gln His	Leu Lys Thr Asn Ser Cys	
	575	580	585
Phe Arg Gly Glu	Arg Gly Lys Ala Phe	Thr Val His His Tyr Ser	
	590	595	600
Gly Glu Val Thr	Tyr Asp Thr Ser Gly	Phe Leu Glu Lys Asn Arg	
	605	610	615
Asp Leu Leu His	Leu Asp Ser Ile Gln	Leu Leu Ser Ser Cys Thr	
	620	625	630
Cys Glu Leu Pro	Gln Ala Phe Ala Ser	Asn Met Leu Ser Leu Ser	
	635	640	645
Glu Lys Pro Val	Pro Gly Pro Leu His	Lys Ser Gly Gly Ala Asp	
	650	655	660
Ser Gln Lys Leu	Ser Val Val Thr Lys	Phe Lys Gly Gln Leu Phe	
	665	670	675
Gln Leu Met Gln	Arg Leu Glu Ser Thr	Thr Pro His Phe Ile Arg	
	680	685	690
Cys Ile Lys Pro	Asn Asn Ser Gln Ser	Pro Gly Ile Tyr His Gln	
	695	700	705
Gly Leu Val Leu	Gln Gln Leu Arg Cys	Cys Gly Val Leu Glu Val	
	710	715	720
Val Arg Ile Ser	Arg Ser Gly Phe Pro	Thr Arg Met Ser His Gln	
	725	730	735
Lys Phe Ala Arg	Arg Tyr Gly Phe Leu	Leu Leu Glu His Val Ala	
	740	745	750
Ser Gln Asp Pro	Leu Ser Val Ser Val	Ala Ile Leu His Gln Phe	
	755	760	765
Asp Ile Leu Pro	Glu Met Tyr Gln Ile	Gly Tyr Thr Lys Leu Phe	
	770	775	780
Phe Arg Thr Gly	Gln Ile Gly Lys Leu	Glu Asp Thr Arg Asn Arg	
	785	790	795
Thr Leu Asn Gly	Ile Leu Arg Val Gln	Ser Cys Phe Arg Gly His	
	800	805	810
Lys Ala Arg Gln	Tyr Met Lys Glu Leu	Lys Arg Gly Ile Phe Asn	
	815	820	825
Leu Gln Ala Phe	Ala Arg Gly Glu Lys	Thr Arg Lys Glu Phe Ala	
	830	835	840
Ile Leu Val His	Arg His Arg Ala Ala	Val His Ile Gln Lys His	
	845	850	855
Ile Lys Ala Lys	Ile Ser Lys Lys Arg	Phe Glu Asp Val His Gly	
	860	865	870
Ala Thr Ile Thr	Leu Gln Ala Val Ile	Arg Gly Trp Leu Val Arg	

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Arg Cys Ser Gly	875	880	885
Asp Ile Ala Leu Leu Gln Phe Gly Ser Gly Lys	890	895	900
Gly Asn Gly Ser Asp Glu Val Leu Val Lys Ser Ser Tyr Leu Ala	905	910	915
Glu Leu Gln Arg Arg Ile Leu Lys Ala Glu Ala Gly Leu Arg Glu	920	925	930
Lys Glu Glu Glu Asn Asp Ile Leu His Gln Arg Leu Gln Gln Tyr	935	940	945
Glu Asn Arg Trp Ser Glu Tyr Glu Leu Lys Met Lys Ser Met Glu	950	955	960
Glu Val Trp Gln Lys Gln Met Arg Ser Leu Gln Ser Ser Leu Ser	965	970	975
Ile Ala Lys Lys Ser Leu Ser Tyr Asp Asp Ser Glu Arg Asn Ser	980	985	990
Asp Ala Ser Ile Asn Thr Ala Asn Asp Glu Thr Asn Pro Pro Trp	995	1000	1005
Asp Ala Ala Thr Asn Gly Arg Arg Asn Gly Val Glu Asn Val Arg	1010	1015	1020
Pro Met Ser Ala Gly Leu Ser Val Ile Ser Arg Leu Ala Glu Glu	1025	1030	1035
Phe Glu Gln Arg Ser Gln Val Phe Gly Asp Asp Ala Lys Phe Leu	1040	1045	1050
Val Glu Val Lys Ser Gly Gln Val Glu Ala Asn Leu Asn Pro Asp	1055	1060	1065
His Glu Leu Arg Arg Leu Lys Gln Met Phe Glu Gly Trp Lys Lys	1070	1075	1080
Asp Tyr Thr Ala Arg Leu Arg Glu Thr Lys Val Ile Leu Asn Lys	1085	1090	1095
Leu Gly His Glu Asp Gly Asp Gly Glu Lys Gly Lys Lys Lys Trp	1100	1105	1110
Trp Gly Arg Leu Asn Ser Ser Arg Val Asn	1115	1120	